

GGAGGGCAGCAAGGACGGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACACCACCGGACAT  
 CTCGGGAGCTGCTGGCTGCAAAGAAGACCCACACCTCACAATTGAAGTGATCCCTTGCAAGATCTGTGG  
 GGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGTGAGGGGTGCAAGGGCTTCTTCCGCCGCAGC  
 CAGCAGTGTAATGTGGCCTACTCCTGCACGCGTCAGCAGAACTGCCCCATTGACCGAACCAGCCGCAACC  
 GATGCCAGCATTGCCGCCTGCAGAAGTGCTGGCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCG  
 AATGTCCAAGAAGCAGAGGGACAGTCTACATGCAGAAGTGCAAAACAAGTGAACAGCAGCAGCAACAG  
 GAACAAGTGGCCAAGACTCCTCCAGCTGGGAGCCGCGGAGCAGACACACTTACATACACTTTAGGGCTCT  
 CAGATGGGCAGCTACCACTGGGCGCCTCACCTGACCTACCCGAGGCCTCTGCTTGTCCCCCTGGCCTCCT  
 GAGAGCCTCAGGCTCTGGCCCACCATATTCCAATACCTTGGCCAAAACAGAGGTCCAGGGGGCCTCCTGC  
 CACCTTGAGTAGTCCAGAACGAGGCAAAGCTGAAGGCAGAGACAGCATCTATAGCACTGACGGCCAAC  
 TTACTCTTGGAAGATGTGGACTTCGTTTTTGAGGAAACCAGGCATCCTGAACTTGGGGAACCAGAACAGGG  
 TCCAGACAGCCACTGCATTCCCAGTTTTCTGCAGTGCCCCAGAGGTACCATATGCCTCTCTGACAGACATA  
 GAGTACCTGGTACAGAATGTCTGCAAGTCCTTCCGAGAGACATGCCAGCTGCGACTGGAGGACCTTCTAC  
 GGCAGCGCACCAACCTCTTTTACGGGAGGAGGTGACAGCTACCAGAGGAAGTCAATGTGGGAGATGTG  
 GGAGCGCTGTGCCACCACCTCACTGAGGCCATTGAGTATGTGGTGGAGTTTGCCAAGCGGCTTTGAGGC  
 TTCATGGAGCTCTGCCAGAATGACCAGATCATACTACTGACAGCAGGAGCAATGGAAGTCGTCTAGTCA  
 GAATGTGCAGGGCCTACAATGCCAACAACCACACAGTCTTTTTTGAAGGCAAATACGGTGGTGTGGAGCT  
 GTTTTCGAGCCTTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCACTTCTCAGCGCCCTG  
 TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCGTCTCTGGGCTCC  
 AAGAGAAGAGGAGAGTGGAAACATCTGCAATACAATTTGGAAGTGGCTTTCCATCATCATCTCTGCAAGAC  
 TCATCGACAAGGCCTCCTAGCCAAGCTGCCACCCAAAGGAAAACCTCCGGAGCCTGTGCAGCCAACATGTG  
 GAAAAGCTGCAGATCTTCCAGCACCTCCACCCCATCGTGGTCCAAGCCGCCTTCCCNCCACTCTATAAGG  
 AACTCTTCAGCACTGATGTTGAATCCCCTGAGGGGCTGTCAAAGTGATCTGGAGGAAGGACAACCTTTCTA  
 TTTCTTCAGCCCTCTGACCCGTCTCCCTGGACTCCCTTACCCAGCCTTTCCCTTTCTGCACTCTATGA  
 AGGGTGGTATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCCTAGGCTTGCCCTTGTTAGGACA  
 ACAGCAGCAAGTGATGGAGAAAAGGCTTGTTATGTTTGATTTCCCATAGTTCACCCCTGGCTTCTGGAA  
 GCTGTGGGGTAGATGGGATAGAGATAGGATGACCAAGTCAAATAAAAAACAGACTGACAATCAGCAGGGA  
 TAAATCCAGGTACCTGGGATAAGGAGAACTCAAATCTAGGCTTGAAAGCTAATAACAGTCCCTTTCAATAC  
 CTCATTGTATTTCCCATGGGTCTCTCTGGGGGACATGGATCTAGCTCAGAGACTGGTGGCAAGCCCCC  
 AGAAGGACCTGTATATAATAAGAATATAGATTCCCTG (SEQ ID NO:1)

MDRAPQRHHRTSRELLAAKKTHTSQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQQCNVAYS  
 CTRQQNCPIDRTSRNRCQHCRLOKCLALGMSRDAVKFGRMSKKQRDSLHAEVQKQLQQQQQQE  
 QVAKTPPAGSRGADTLTYTLGLSDGQLPLGASPDLPASACPPGLLRASGSGPPYSNTLAKTEVQG  
 ASCHLEYSPERGKAEGRDSIYSTDGQLTLGRCGLRFEETRHPPELGEPEQGPDSHCIPSFCSPAEPY  
 ASLTDIEYL VQNVCKSFRETCLRLDLLRQRTNLFSSREEVTSYQRKSMWEMWERCAHHLTEAIQ  
 YVVEFAKRLSGFMELCQNDQILLTAGAMEVVLVRMCRAYNANNHTVFFEGKYGGVELFRALGC  
 SELISSIFDFSHFLSALCFSEDEIALYTALVLINANRPGLEKRRVEHLQYNLELAFHHHLCKTHRQG  
 LLAKLPKGLRLSLCSQHVEKLQIFQHLHPVVQAAPPLYKELFSTDVESPEGLSK (SEQ ID NO:2)

FIG. 1

underlined = deleted in targeting construct

green = sequence flanking Neo insert in targeting construct

GGAGGGCAGCAAGGACGGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACAC  
CACCGGACATCTCGGGAGCTGCTGGCTGCAAAGAAGACCCACACCTCACAAATTGAAGTG  
ATCCCTTGCAAGATCTGTGGGGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGT  
GAGGGGTGCAAG [ GGCTTCTTCCGCCGAGCCAGCAGTGTAATGTGGCCTACTCCTGCACG  
CGTCAGCAGAA ] CTGCCCCATTGACCGAACCAGCCGCAACCGATGCCAGCATTGCCGCCTG  
CAGAAGTGCCTGGCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCGAATGTCCAAG  
AAGCAGAGGGACAGTCTACATGCAGAAGTGCAGAAACAACCTGCAACAGCAGCAGCAACAG  
GAACAAGTGGCCAAAGACTCCTCCAGCTGGGAGCCGCGGAGCAGACACACTTA [ CATACACT  
TTAGGGCTCTCAGATGGGCAGCTACCACTGGGCGCCTCACCTGACCTACCCGAGGCCTCT  
GCTTGTCCCCCTGGCCTCCTGAGAGCCTCAGGCTCTGGCCCACCATATTCCAATACCTTG  
GCCAAAACAGAGGTCCAGGGGGCCTCCTGCCACCTTGAGTATAGTCCAGAACGAGGCAAA  
GCTGAAGGCAGAGACAGCATCTATAGCACTGACGGCCAACCTTACTCTTGGAAGATGTGGA  
CTTCGTTTTGAGGAAACCAGGCATCCTGAACCTTGGGGAACCAGAACAGGGTCCAGACAGC  
CACTGCATTCCCAGTTTCTGCAGTGGCCAGAGGTACCATATGCCTCTCTGACAGACATA  
G ] AGTACCTGGTACAGAATGTCTGCAAGTCCCTTCCGAGAGACATGCCAGCTGCGACTGGAG  
GACCTTCTACGGCAGCGCACCAACCTCTTTTCACGGGAGGAGGTGACCAGCTACCAGAGG  
AAGTCAATGTGGGAGATGTGGGAGCGCTGTGCCACCACCTCACTGAGGCCATTTCAGTAT  
GTGGTGGAGTTTGCCAAGCGGCTTTTCAGGCTTCATGGAGCTCTGCCAGAATGACCAGATC  
ATACTACTGACAGCAGGAGCAATGGAAGTCGTCCTAGTCAGAATGTGCAGGGCCTACAAT  
GCCAACAAACCACACAGTCTTTTTTGAAGGCAATACGGTGGTGTGGAGCTGTTTCGAGCC  
TTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCCTTCTCAGCGCCCTG  
TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCGT  
CCTGGGCTCCAAGAGAAGAGGAGAGTGGAACATCTGCAATACAATTTGGAAGTGGCTTTC  
CATCATCATCTCTGCAAGACTCATCGACAAGCCTCCTAGCCAAGCTGCCACCCAAAGGA  
AAAC TCCGGAGCCTGTGCAGCCAACATGTGGAAGAGCTGCAGATCTTCCAGCACCTCCAC  
CCCATCGTGGTCCAAGCCGCTTCCNCCACTCTATAAGGAACTCTTCAGCACTGATGTT  
GAATCCCCCTGAGGGGCTGTCAAAGTGATCTGGAGGAAGGACAACCTTCTATTTCCCTCAG  
CCCTCTGACCCGCTCTCCCTGGACTCCCTTCAACCAGCCTTTCCCTTTCTGCACTCTATGA  
AGGGTGGTATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCCCTAGGCTTGCC  
TTGTAGGACAACAGCAGCAAGTGATGGAGAAAAGGCTTGTTATGTTTGATTTCCCATAG  
TTCCACCCTGGCTTCTGGAAGCTGTGGGGTAGATGGGATAGAGATAGGATGACCAAGTCA  
AATAAAAAACAGACTGACAATCAGCAGGGATAAATCCAGGTACCTGGGATAAGGAGAACT  
CAAATCTAGGCTTGAAAGCTAATAACAGTCCCTTCAATACCTCATTGTATTTCCCCATGG  
GTCTCTCTGGGGGGACATGGATCTAGCTCAGAGACTGGTGGCAAGCCCCCAGAAGGACCT  
GTATATAATAAGAATATAGATTCCCTG (SEQ ID NO:1)

FIG. 2A

Gene Sequence  
Structure \*

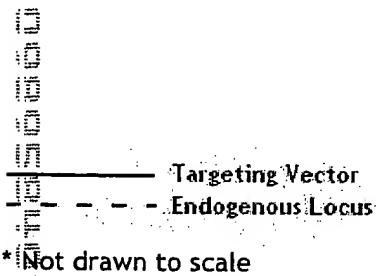
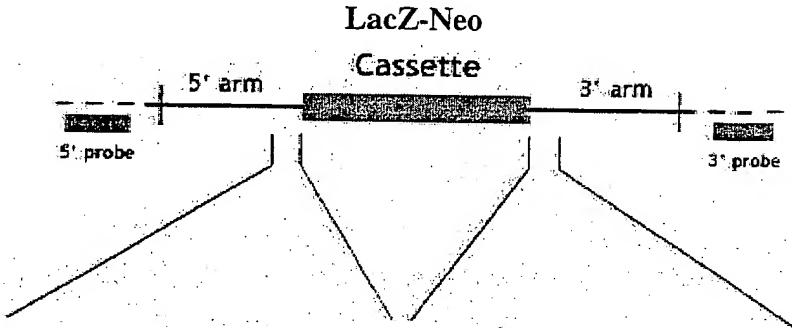
252 bp      Sequence Deleted      472 bp

Size of full-length  
cDNA: 2066 bp



Targeting Vector\* (genomic sequence)  
Construct Number: 651

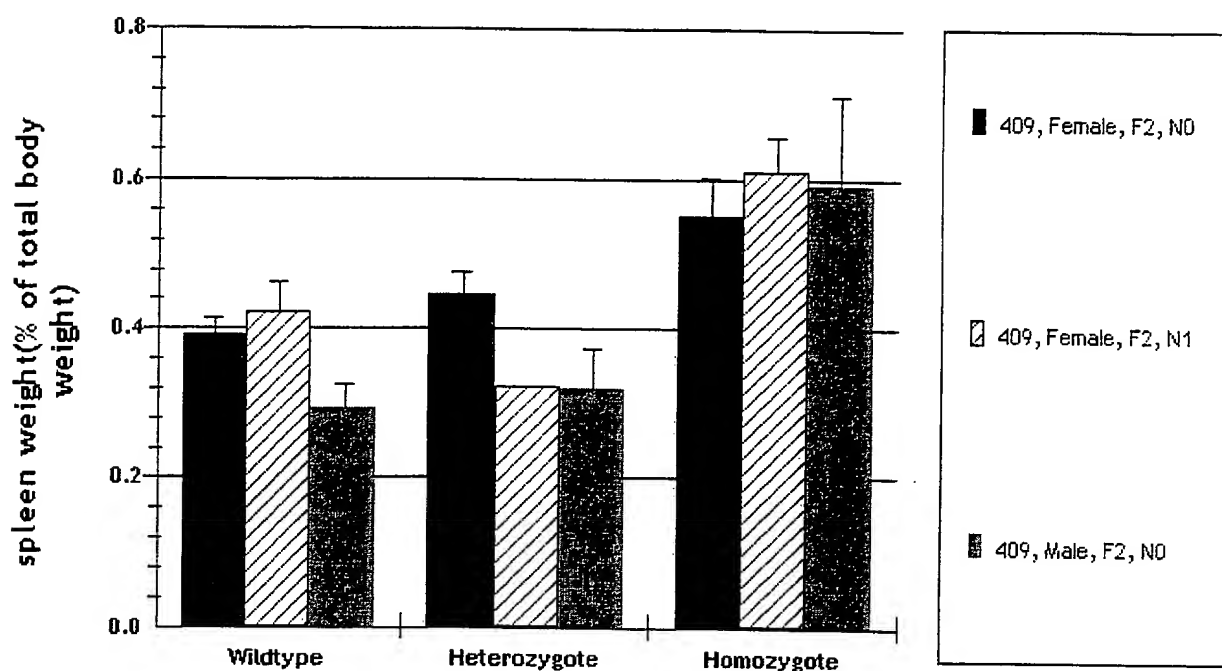
Arm Length:  
5': 1.6 kb  
3': 2.5 kb



5'>CAGGGTCCATCACAATTATAC AGTGGAGGTTCTGGGGACTTTGGTG GATGTAGAAATTCTTGAGACCAGT GCACATGAATTGGAGGTCCCTGGG ACCACCTCAAACCTCCGAGAGGGTG GGATAAGCAGTTTCTGTTTCCCAG GGCTTCTTCCGCCGCAGCCAGCAG TGTAATGTGGCCTACTCCTGCACG CGTCAGCAGAA<3' (SEQ ID NO: 3)	5'>CATACACTTTAGGGCTCTCAG ATGGGCAGCTACCACTGGGCGCCT CACCTGACCTACCCGAGGCCTCTG CTTGTCCTCCCTGGCCTCCTGAGAG CCTCAGGCTCTGGCCCACCATATT CCAATACCTTGGCCAAAACAGAGG TCCAGGGGGCCTCCTGCCACCTTG AGTATAGTCCAGAACGAGGCAAAG CTGAAGGCAGA<3' (SEQ ID NO: 4)
--	---

FIG. 2B

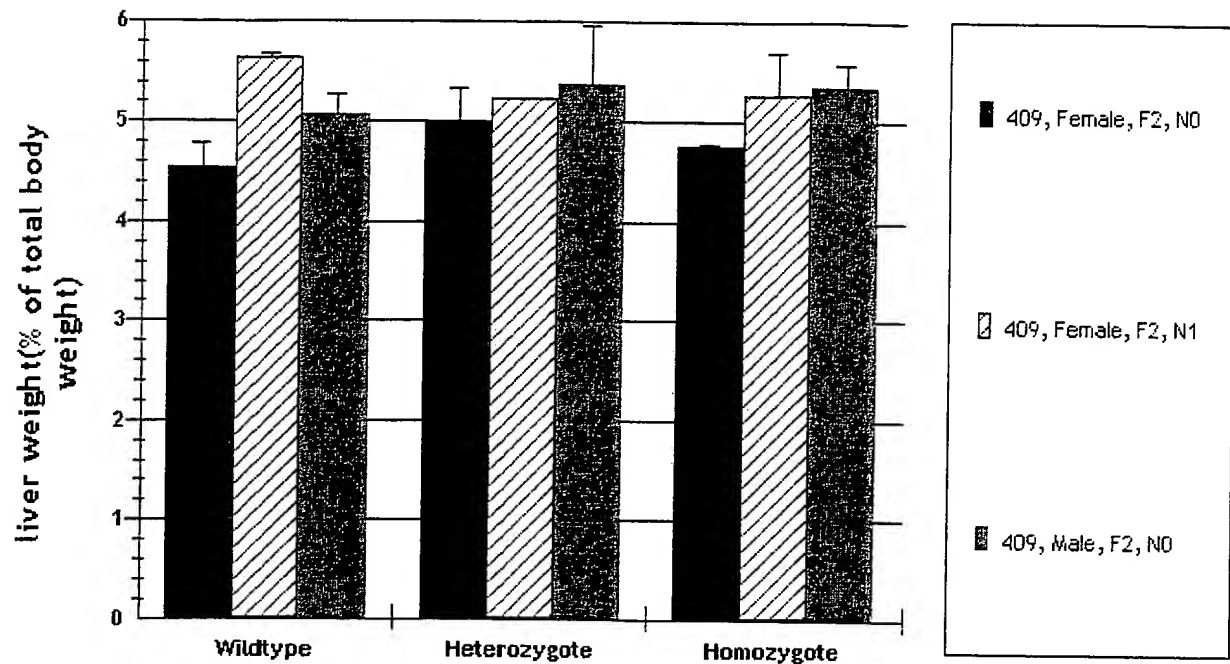
## necropsy - spleen weight/body weight



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FIG. 3

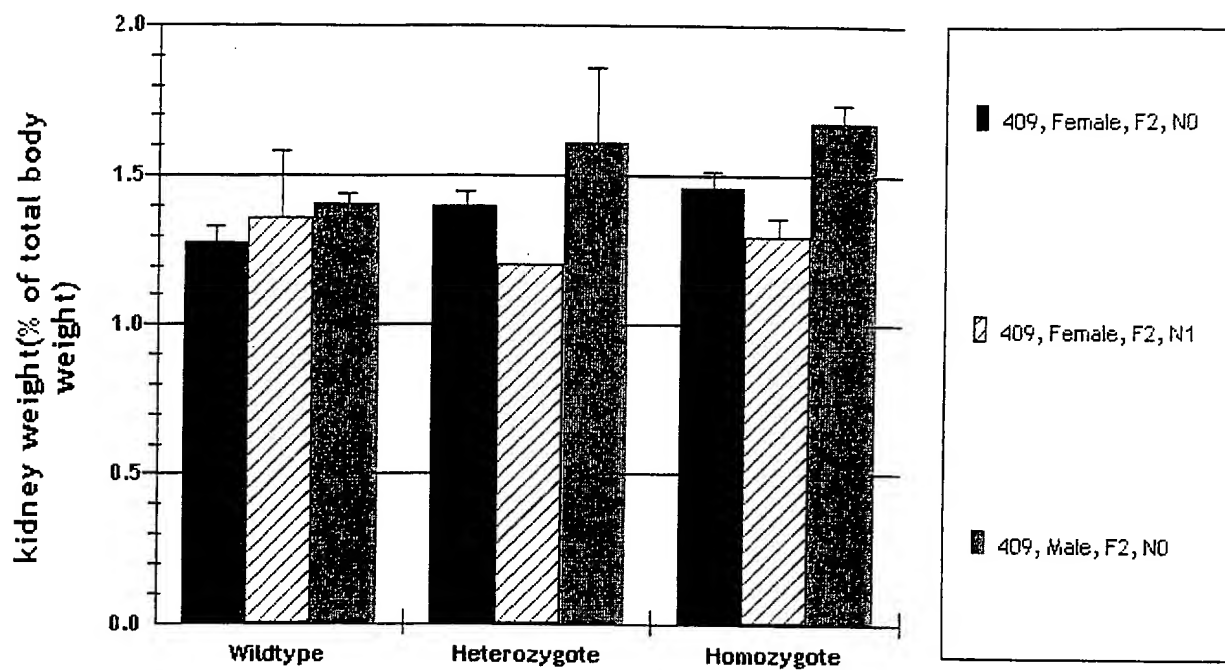
## necropsy - liver weight/body weight



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FIG. 4

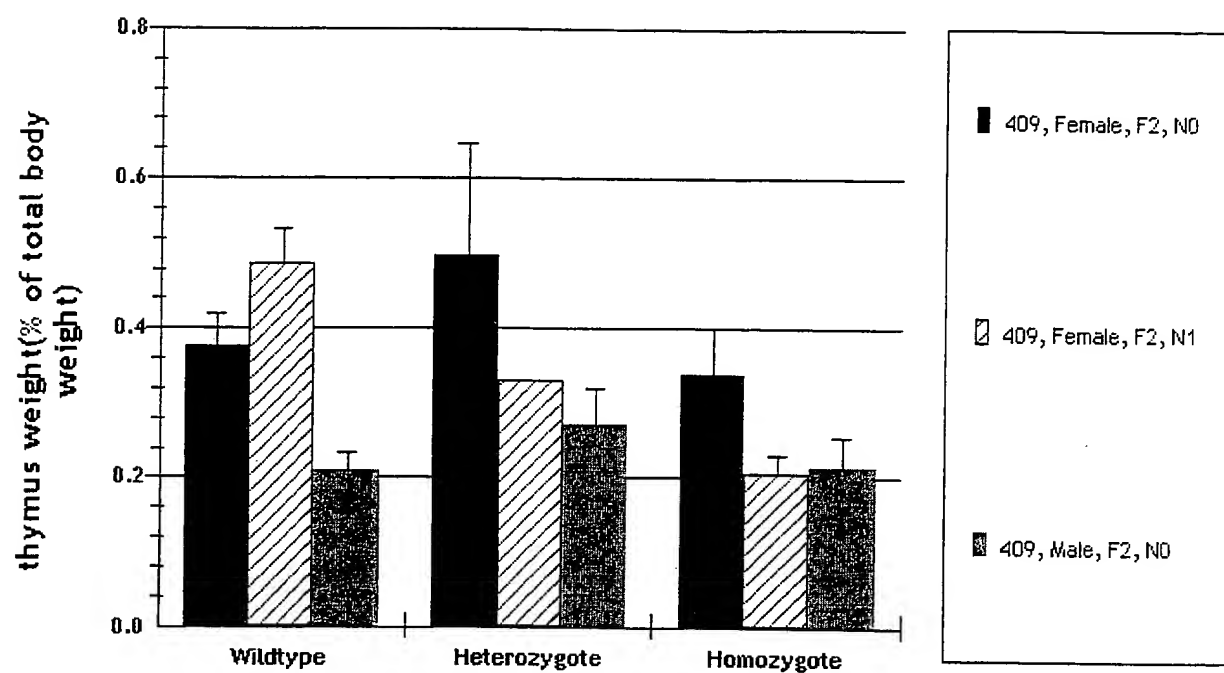
## necropsy - kidney weight/body weight



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FIG. 5

## necropsy - thymus weight/body weight



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FIG. 6